

NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUEECNES ENCODING SAME

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REPLACEMENT SHEET

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Fig. 1A

- 60	tgaaaagatagaataaatggcctcgtg
1	<u>ATGGCGCGGCCAGCGCTGCTGGGCGAG</u>
1	M A R P A L L G E
61	<u>GGCCAAGTTGCCGCGGCCACAGAAGTT</u>
21	G Q V A A A T E V
121	GAAAATCTCTGCACGATAATATGGACG
41	E N L C T I I W T
181	ACTCTCAGATATTTTAGTCACTTTGAT
61	T L R Y F S H F D
241	CATCGTAAAGAGGAATTACCCCTGGAT
81	H R K E E L P L D
301	AGTGCCAATGAAAGTGAGAAGCCTAGC
101	S A N E S E K P S
361	GGTGATCCTGAGTCCGCTGTGACTGAG
121	G D P E S A V T E
421	AAGTGTTTCCTGGCTCCCTGGAAGGAAT
141	K C S W L P G R N

Fig. 1 B

ccgaattcggcacgagccgagggcgaggggcctgc

CTGTTGGTGCTGCTACTGTGGACCGCCACCGTG

L L V L L L W T A T V

CAGCCACCTGTGACGAATTTGAGCGTCTCTGTC

Q P P V T N L S V S V

TGGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC

W S P P E G A S P N C

GACCAACAGGATAAGAAAATTGCTCCAGAAACT

D Q Q D K K I A P E T

GAGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT

E K I C L Q V G S Q C

CCTTTGGTGAAAAAGTGCATCTCACCCCTGAA

P L V K K C I S P P E

CTCAAGTGCATTTGGCATAACCTGAGCTATATG

L K C I W H N L S Y M

ACAAGCCCTGACACACACTATACTCTGTACTAT

T S P D T H Y T L Y Y

Fig. 1c

481	TGGTACAGCAGCCTGGACAAAAGTCGT
161	W Y S S L E K S R
541	ATTGCTTGTTTCCTTTAAATTGACTAAA
181	I A C S F K L T K
601	ATAATGGTCAAGGATAATGCTGGGAAA
201	I M V K D N A G K
661	TCCTATGTGAAACCTGATCCTCCACAT
221	S Y V K P D P P H
721	TTAGTGCAGTGGAAGAATCCACAAAAT
241	L V Q W K N P Q N
781	GTCAATAATACTCAAACCGACCGACAT
261	V N N T Q T D R H
841	AATTCCGAATCTGATAGAAACATGGAG
281	N S E S D R N M E
901	GCCGACGCTGTCTACACAGTCAGAGTA
301	A D A V Y T V R V
961	AACAAACTGTGGAGTGATTGGAGTGAA
321	N K L W S D W S E

Fig. 1 D

CAATGTGAAAACATCTATAGAGAAGGTCAACAC
Q C E N I Y R E G Q H

GTGGAACCTAGTTTTGAACATCAGAACGTTCAA
V E P S F E H Q N V Q

ATTAGGCCATCCTGCAAAATAGTGTCTTTAACT
I R P S C K I V S L T

ATTAAACATCTTCTCCTCAAAAATGGTGCCTTA
I K H L L L K N G A L

TTTAGAAGCAGATGCTTAACTTATGAAGTGGAG
F R S R C L T Y E V E

AATATTTTAGAGGTTGAAGAGGACAAATGCCAG
N I L E V E E D K C Q

GGTACAAGTTGTTTCCAACCTCCCTGGTGTCTT
G T S C F Q L P G V L

AGAGTCAAAACAAACAAGTTATGCTTTGATGAC
R V K T N K L C F D D

GCACAGAGTATAGGTAAGGAGCAAAACTCCACC
A Q S I G K E Q N S T

Fig. 1 E

1021	<u>TTCTACACCACCATGTTACTCACCATT</u>
341	<u>F Y T T M L L T I</u>
1081	<u>CTTTT</u> <u>TACCTGAAAAGGCTTAAGATC</u>
361	<u>L F Y L K R L K I</u>
1141	ATTTTAAAGAAATGTTTGGAGACCAG
381	I F K E M F G D Q
1201	ATCTATGAGAAACAATCCAAAGAAGAA
401	I Y E K Q S K E E
1261	AAAGCAGCTCCTTGAtgggggagaagtg
421	K A A P *
1321	gatttattgcattctccatttgttatc
1381	cttgaaaaacaggcagctcctaagagc
1441	ccaaacccaaaggagctccttccaaga
1501	ccctaaaagcagatgttttgccaaatc
1561	accatcaattcatctaatacaggaattg

Fig. 1 F

CCAGTCTTTGTCGCAGTGGCAGTCATAATCCTC
P V F V A V A V I I L

ATTATATTTCTCCAATTCCTGATCCTGGCAAG
I I F P P I P D P G K

AATGATGATACCCTGCACTGGAAGAAGTATGAC
N D D T L H W K K Y D

ACGGATTCTGTAGTGCTGATAGAAAACCTGAAG
T D S V V L I E N L K

atttcttttcttgccttcaatgtgaccctgtgaa

tgggggacttggttaaataagaaactgaaactact
cacaggtcttgatgtgacttttgcattgaaaac
aaagcaagagttcttctcgttccttggtccaat
cccaaactagaggacaaagacaaggggacaatg
tgatggcttcctaaggaatctctgcttgctctg

Fig. 1 G